

SEQUENCE LISTING

<110> Barnett, Susan
Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> 1631.002

<140>

<141>

<150> 60/152,195

<151> 1999-09-01

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 1

gacatcaagc agggccccaaggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 2

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 2

gacatccgcc agggccccaaggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 3

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110965

<400> 3

atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tgggtgtgggc cagccgcgag 120
ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
atccgccagc tgcacccgc cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
accgtggcca ccctgtactg cgtgcacgag aagatcgagg tccgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggtgat cgaggagaag 480

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gccttcagcc ccgaggtgat ccccatgttc accgccctga gcgagggcgc cccccccag 540
gacctgaaca cgatgttgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
gacaccatca acgaggaggc cgccgagtgg gaccgcgtgc accccgtgca cgccggcccc 660
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aagcgggtgga tcatcctggg cctgaacaag atcgtgcgga tgtacagccc cgtgagcatc 840
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tgccgcgccc ccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
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cccggcaact tctgcagag ccgccccgag cccaccgccc ccccgccga gagcttccgc 1380
ttcaggagga ccaccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgaccccctg agccagtaa 1479

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<210> 4

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110967

<400> 4

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ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tgggtgtggc cagccgcgag 120
ctggaggggt tgcacctgaa ccccgccctg ctggagaccg ccgagggctg caagcagacc 180
atgaagcagc tgcagccgcg cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
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gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac ccccaggac 540
ctgaacacga tgttgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
gcccccgccc agatgcgcga ccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac cccccgtgc ccgtgggcga catctacaag 780
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cagaacgcca acccgcactg caagaccatc ctgcgcgctc tcggccccgg cgccaccctg 1020
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gccgaggcga tgagccaggc caacagcgtg aacatcatga tgcagaagag caacttcaag 1140
ggcccccgcc gcaacgtcaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
tgccgcgccc ccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgcaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
cccggcaact tctgcagaa ccgcagcgag cccgcgccc ccaccgtgcc caccgcccc 1380
cccgcgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gcccaaggac 1440
cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggccccctg 1500
agccagtaa 1509

```

<210> 5
 <211> 141
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Env common
 region of HIV strain AF110968

<400> 5

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accatcacca tcacctgccg catcaagcag atcatcaaca tgtggcagaa ggtgggcccgc 60
gccatgtacg ccccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
ctgctgaccc gcgacggcgg c                                     141
```

<210> 6
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
 gp120 coding region of HIV strain AF110968

<400> 6

```
agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgctgaccc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aaggggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccg aggcctgccc caagggtgagc 540
ttcgacccca tccccatcca ctactgcacc ccgcgcggct acgccatcct gaagtgcac 600
aaccagacct tcaacggcac cggccccctg aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag caccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcac 840
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gagcacttca gcaagaaggc catcaagttc gagcccagca gcggcggcga cctggagatc 1020
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aacagcacct acagccccag cttcaacggc accgagaaca agctgaacgg caccatcacc 1140
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atgcgcgaca actggcgcaa cgagctgtac aagtacaagg tggaggagat caagccccctg 1380
ggcgtggccc ccaccgaggc caagcgccgc gtggtggagc gcgagaagcg c                                     1431
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<210> 7
 <211> 1944
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110968

<400> 7

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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccg aggcctgccc caaggtgagc 540
ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag caccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcac 840
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gagcacttca gcaagaaggc catcaagttc gagcccagca gcggcggcga cctggagatc 1020
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aacagcacct acagccccag cttcaacggc accgagaaca agctgaacgg caccatcacc 1140
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agcaaccgca gccacgacga gatctgggac aacatgacct ggatgcagtg ggaccgcgag 1800
atcaacaact acaccgacac catctaccgc ctgctggagg agagccagaa ccagcaggag 1860
aagaacgaga aggacctgct ggccctggac agctggcaga acctgtggaa ctggttcagc 1920
atcaccaact ggctgtggta catc 1944

<210> 8

<211> 2466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110968

<400> 8

agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300

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ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcgga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccg aggcctgccc caaggtgagc 540
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aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag caccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
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cgcatctgcc gcgccatccg caacatcccc cgccgcatcc gccagggctt cgaggccgcc 2460
ctgcag 2466

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<210> 9

<211> 2547

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110968

<400> 9

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ttctggatgc tgatcatcag cagcgtggtg ggcaacctgt gggtagacct gtactacggc 120
gtgcccgtgt ggaaggaggc caagaccacc ctgttctgca ccagcgacgc caaggcctac 180
gagaccgagg tgcaaacgt gtgggccacc cagcctgccc tgcccaccga ccccaacccc 240
caggagatcg tgtggagaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300

```

```

gaccagatgc acgaggacat catcagcctg tgggaccaga gcctgaagcc ctgCGTgaag 360
ctgaccccc tgtgCGtgac cctgaagtgc cgcaacgtga acgccacca caacatcaac 420
agcatgatcg acaacagcaa caagggcgag atgaagaact gcagcttcaa cgtgaccacc 480
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gtgcgccagg gctacagccc cctgccccct cagacctga ccccaacc cgcgagccc 2160
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aagaagagcg ccatcagcct gctggacacc atcgccatcg cgtggccga gggcaccgac 2460
cgcatcatcg agttcatcca gcgcatctgc cgcgccatcc gcaacatccc cgcgCGcatc 2520
cgccagggct tcgaggccgc cctgcag 2547

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<210> 10
 <211> 1035
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic a
 gp41 coding region of HIV strain AF110968

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<400> 10
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cagaacaacc tgcTgcgCGc catcagaggcc cagcagcacc tgcTgcagct gaccgtgtgg 180
ggcatcaagc agctgcagac cgcacatcctg gccgtggagc gctacctgaa ggaccagcag 240
ctgctgggca tctggggcgt cagcggcaag ctgatctgca ccaccgCGgt gccctggaac 300

```

```

agcagctgga gcaaccgcag ccacgacgag atctgggaca acatgacctg gatgcagtgg 360
gaccgcgaga tcaacaacta caccgacacc atctaccgcc tgctggagga gagccagaac 420
cagcaggaga agaacgagaa ggacctgctg gccctggaca gctggcagaa cctgtggaac 480
tggttcagca tcaccaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcgccc tgcgcatcat ctctgcctg ctgagcatcg tgaaccgcgt gcgccagggc 600
tacagcccc tgccttcca gacctgacc cccaaccccc gcgagcccga ccgcctgggc 660
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gaggccgccc tgcag                                     1035

```

<210> 11

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Env
common region of HIV strain AF110975

<400> 11

```

agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg cccgcgacgg cggc                                     144

```

<210> 12

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110975

<400> 12

```

agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
agaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgccctt gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaaacaagg ccgtgcagcg cgtgagcggc 960

```

aagctgcgcg	agcaacttccc	caacaagacc	atcgagttcc	agcccagcag	cggcggcgac	1020
ctggagatca	ccacccacag	cttcaactgc	cgcggcgagt	tcttctactg	caacaccagc	1080
aagctgttca	acagcagcta	caacggcacc	agctaccgcg	gcaccgagag	caacagcagc	1140
atcatcacc	tgccttgcgc	catcaagcag	atcatcgaca	tgtggcagaa	ggtgggcccgc	1200
gccatctacg	cccccccat	cgagggcaac	atcacctgca	gcagcagcat	caccggcctg	1260
ctgctggccc	gcgacggcgg	cctggacaac	atcaccaccg	agatcttccg	ccccaggggc	1320
ggcgacatga	aggacaactg	gcgcaacgag	ctgtacaagt	acaaggtggt	ggagatcaag	1380
cccctgggcg	tggccccccac	cgaggccaag	cgccgcgtgg	tggagcgcg	gaagcgc	1437

<210> 13

<211> 1950

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110975

<400> 13

agcggcctgg	gcaacctgtg	ggtgaccgtg	taegacggcg	tgccctgtgt	gcgcgaggcc	60
agcaccacc	tgttctgcgc	cagcgacgcc	aaggcctacg	agaaggaggt	gcacaacgtg	120
tggggcacc	acgcctgcgt	gccaccgac	cccaaccccc	aggagatcga	gctggacaac	180
gtgaccgaga	acttcaacat	gtggaagaac	gacatggtgg	accagatgca	cgaggacatc	240
atcagcctgt	gggaccagag	cctgaagccc	cgcggtgaagc	tgacccccct	gtgcgtgacc	300
ctgaagtgca	ccaactacag	caccaactac	agcaaacacca	tgaacgccac	cagctacaac	360
aacaacacca	ccgaggagat	caagaactgc	accttcaaca	tgaccacoga	gctgcgcgac	420
aagaagcagc	aggtgtacgc	cctgttctac	aaegtggaca	tcgtgcccct	gaacagcaac	480
agcagcgagt	accgcctgat	caactgcaac	accagcgcca	tcaccaggc	ctgccccaa	540
gtgagcttcg	accccatccc	catccactac	tgcgcccccg	ccggctacgc	catcctgaag	600
tgcaagaaca	acaccagcaa	cggcaccggc	ccctgccaga	acgtgagcac	cgtgcagtgc	660
acccacggca	tcaagcccg	ggtgagcacc	ccctgctgc	tgaacggcag	cctggccgag	720
ggcggcgaga	tcatcatccg	cagcaagaac	ctgagcaaca	acgcctacac	catcatcgtg	780
cacctgaacg	acagcgtgga	gatcgtgtgc	acccgcccc	acaacaacac	ccgcaagggc	840
atccgcatcg	gccccggcca	gaccttctac	gccaccgaga	acatcatcgg	cgacatccgc	900
caggcccaact	gcaacatcag	cgccggcgag	tggacaag	ccgtgcagcg	cgtgagcgcc	960
aagctgcgcg	agcaacttccc	caacaagacc	atcgagttcc	agcccagcag	cggcggcgac	1020
ctggagatca	ccacccacag	cttcaactgc	cgcggcgagt	tcttctactg	caacaccagc	1080
aagctgttca	acagcagcta	caacggcacc	agctaccgcg	gcaccgagag	caacagcagc	1140
atcatcacc	tgccttgcgc	catcaagcag	atcatcgaca	tgtggcagaa	ggtgggcccgc	1200
gccatctacg	cccccccat	cgagggcaac	atcacctgca	gcagcagcat	caccggcctg	1260
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ggcgacatga	aggacaactg	gcgcaacgag	ctgtacaagt	acaaggtggt	ggagatcaag	1380
cccctgggcg	tggccccccac	cgaggccaag	cgccgcgtgg	tggagcgcg	gaagcgcgc	1440
gtgggcatcg	gcgcctgat	cttcggcttc	ctgggcgcgc	ccggcagcaa	catgggcgc	1500
gccagcatca	ccctgaccgc	ccaggcccgc	cagctgctga	gcggcatcgt	gcagcagcag	1560
agcaacctgc	tgcgcgccat	cgaggcccag	cagcacatgc	tgacgtgac	cgtgtggggc	1620
atcaagcagc	tgcaggcccg	cgtgctggcc	atcgagcgct	acctgaagga	ccagcagctg	1680
ctgggcatct	ggggctgcag	cggcaagctg	atctgcacca	ccaccgtgcc	ctggaacagc	1740
agctggagca	acaagaccca	gggcgagatc	tgggagaaca	tgacctggat	gcagtgggac	1800
aaggagatca	gcaactacac	cggcatcatc	taccgcctgc	tggaggagag	ccagaaccag	1860
caggagcaga	acgagaagga	cctgctggcc	ctggacagcc	gcaacaacct	gtggagctgg	1920
ttcaacatca	gcaactggct	gtggtacatc				1950

<210> 14

<211> 2493
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
 gp160 coding region of HIV strain AF110975

<400> 14

```

agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatgggtg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgctgaagc tgacccccct gtgctgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgccccct gaacagcaac 480
agcagcagat accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaa 540
gtgagcttcg accccatccc catccactac tgcccccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc cctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc accgccccca acaacaacac ccgcaagggc 840
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caggcccaact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
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ctgcagcgcg gctgggaggg cctgaagtac ctgggcagcc tgggtgcagta ctggggcctg 2340
gagctgaaga agagcgccac cagcctgctg gacagcatcg ccatcgccgt ggccgagggc 2400
accgaccgca tcatcgaggt gatccagcgc atctaccgcg ccttctgcaa catccccgcg 2460
cgctgcgcgc agggcttcga ggccgcctcg cag 2493

```

<210> 15
 <211> 2565

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110975

<400> 15

```
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ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120
tggcgcgagg ccagcaccac cctgttctgc gccagcgacg ccaaggccta cgagaaggag 180
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagatc 240
gagctggaca acgtgaccga gaacttcaac atgtggaaga acgacatggg ggaccagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cccgcgtgaa gctgaccccc 360
ctgtgcgtga ccctgaagtg caccaactac agcaccaact acagcaacac catgaacgcc 420
accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc 480
gagctgcgcg acaagaagca gcaggtgtac gccctgttct acaagctgga catcgtgccc 540
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gcctgcccc aagtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660
gccatcctga agtgcaagaa caacaccagc aacggcaccg gccctgcca gaacgtgagc 720
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tactggggcc tggagctgaa gaagagcgcc accagcctgc tggacagcat cgccatcgcc 2460
gtggccgagg gcaccgaccg catcatcgag gtgatccagc gcatctaccg cgccttctgc 2520
aacatcccc gccgcgtgcg ccagggcttc gaggccgccc tgacg 2565
```

<210> 16

<211> 1056
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic a
 gp41 coding region of HIV strain AF110975

<400> 16

```

gccgtgggca tcggcgccgt gatcttcggc ttcttgggcg ccgcccgcag caacatgggc 60
gccgccagca tcacctgac cgcccaggcc cgccagctgc tgagcggcat cgtgcagcag 120
cagagcaacc tgctgcgcgc catcgaggcc cagcagcaca tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcaggc ccgctgtctg gccatcgagc gctacctgaa ggaccagcag 240
ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccaccgt gccctggaac 300
agcagctgga gcaacaagac ccagggcgag atctgggaga acatgacctg gatgcagtgg 360
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cagcaggagc agaacgagaa ggacctgtg gccctggaca gccgcaaca cctgtggagc 480
tggttcaaca tcagcaactg gctgtgttac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcggcc tgcgcacatc cttcgccgtg ctgagcatcg tgaaccgcgt gcgccaggcc 600
tacagccccc tgagcttcca gaccctgacc cccaaccccc gcggcctgga ccgcctgggc 660
cgcatcgagg agggggcgcg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
ttcttgccc tggcctggga cgacctgcgc agcctgtgcc tgttcagcta ccaccgcctg 780
cgcgacctga tcttggtgac cgcccgctg gtggagctgc tgggcccag cagccccgcg 840
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ctggagctga agaagagcgc caccagcctg ctggacagca tcgccatcgc cgtggccgag 960
ggcaccgacc gcatcatcga ggtgatccag cgcattctacc gcgccttctg caacatcccc 1020
cgccgcgtgc gccagggctt cgaggccgcc ctgcag 1056
  
```

<210> 17

<211> 492

<212> PRT

<213> Human immunodeficiency virus

<400> 17

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Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
  1             5             10             15

Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
  20             25             30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
  35             40             45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
  50             55             60

His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
  65             70             75             80

Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
  85             90             95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
  100            105            110
  
```

Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln
 115 120 125
 Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala
 130 135 140
 Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys
 145 150 155 160
 Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly
 165 170 175
 Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His
 180 185 190
 Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala
 195 200 205
 Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly
 210 215 220
 Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
 225 230 235 240
 Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val
 245 250 255
 Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val
 260 265 270
 Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys
 275 280 285
 Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala
 290 295 300
 Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu
 305 310 315 320
 Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly
 325 330 335
 Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly
 340 345 350
 Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala
 355 360 365
 Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
 370 375 380
 Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
 385 390 395 400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
405 410 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
420 425 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
435 440 445

Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
450 455 460

Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser
465 470 475 480

Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln
485 490

<210> 18

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110968

<400> 18

atgcgcgtga tgggcatcct gaagaactac cagcagtggt ggatgtgggg catcctgggc 60
ttctggatgc tgatcatcag c 81

<210> 19

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110975

<400> 19

atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gc 72

<210> 20

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
coding sequence of HIV strain AF110965

<400> 20

```
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ctggagaagt tcgccctgaa ccccgccctg ctggagacca gcgagggctg caagcagatc 180
atccgccagc tgcaccccg cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
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ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgctg agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggtgat cgaggagaag 480
gccttcagcc ccgaggtgat ccccatgttc accgcctga gcgagggcgc cccccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
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ctggccgagg ccatgagcca ggccaacacc agcgtgatga tgcagaagag caacttcaag 1140
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tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttctct ggcaagatct ggcccagcca caagggccgc 1320
cccggcaact tcctgcagag ccgccccgag cccaccgccc ccccgccga gagcttccgc 1380
ttcgaggaga ccacccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgacccccct agccagtaa 1479
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<210> 21

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag coding sequence of HIV strain AF110967

<400> 21

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ctgcccccg ggcgcaagaa gcactacatg ctgaagcacc tgggtgtggc cagccgcgag 120
ctggagggct tcgccctgaa ccccgccctg ctggagaccg ccgagggctg caagcagatc 180
atgaagcagc tgcagcccg cctgcagacc ggcaccgagg agctgcgag cctgtacaac 240
accgtggcca ccctgtactg cgtgcacgcc ggcacgagg tgcgagacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag agccagcaga agaccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac cccccaggac 540
ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgctgcacc ccgtgcaggc cggccccgtg 660
gccccggccc agatgcgaga ccccgccg gcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac cccccgtgc ccgtgggcga catctacaag 780
cgctggatca tcctgggccc gaacaagatc gtgcgcatgt acagccccgt gagcatcctg 840
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
cagaacgcca accccgactg caagaccatc ctgcgcgccc tgggcccccg cgccaccctg 1020
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gaggagatga tgaccgcctg ccagggcgctg ggcggccccc gccacaaggc ccgcgtgctg 1080
 gccgaggcca tgagccaggc caacagcgctg aacatcatga tgcagaagag caacttcaag 1140
 ggcccccgcc gcaacgtgaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
 tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
 gactgcaccg agcgccaggc caacttctg ggcaagatct ggcccagcca caagggccgc 1320
 cccggcaact tcctgcagaa ccgcagcgag cccgccgccc ccaccgtgcc caccgcccc 1380
 cccgccgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gccaaggac 1440
 cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tggtcggcag cggccccctg 1500
 agccagtaa 1509

<210> 22

<211> 502

<212> PRT

<213> Human immunodeficiency virus

<400> 22

Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
 50 55 60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
 100 105 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
 115 120 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
 130 135 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
 145 150 155 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
 165 170 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
 180 185 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
 195 200 205

Trp Asp Arg Leu His Pro Val Gln Ala Gly Pro Val Ala Pro Gly Gln
 210 215 220
 Met Arg Asp Pro Arg Gly Ser Asp Ile Ala Gly Ala Thr Ser Thr Leu
 225 230 235 240
 Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Val Pro Val Gly
 245 250 255
 Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
 260 265 270
 Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
 275 280 285
 Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
 290 295 300
 Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
 305 310 315 320
 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
 325 330 335
 Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
 340 345 350
 Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn
 355 360 365
 Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
 370 375 380
 Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
 385 390 395 400
 Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
 405 410 415
 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
 420 425 430
 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
 435 440 445
 Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
 450 455 460
 Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
 465 470 475 480
 Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
 485 490 495

Ser Gly Pro Leu Ser Gln
500

<210> 23
<211> 849
<212> PRT
<213> Human immunodeficiency virus

<400> 23
Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
35 40 45

Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp
130 135 140

Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr
145 150 155 160

Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu
165 170 175

Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile
180 185 190

Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
195 200 205

Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu
210 215 220

Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val
225 230 235 240

Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln
 245 250 255
 Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser
 260 265 270
 Glu Asn Leu Ala Asn Asn Ala Lys Ile Ile Ile Val Gln Leu Asn Lys
 275 280 285
 Pro Val Lys Ile Val Cys Val Arg Pro Asn Asn Asn Thr Arg Lys Ser
 290 295 300
 Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile
 305 310 315 320
 Gly Asp Ile Arg Gln Ala Tyr Cys Ile Ile Asn Lys Thr Glu Trp Asn
 325 330 335
 Ser Thr Leu Gln Gly Val Ser Lys Lys Leu Glu Glu His Phe Ser Lys
 340 345 350
 Lys Ala Ile Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
 355 360 365
 Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Ser
 370 375 380
 Gln Leu Phe Asn Ser Thr Tyr Ser Pro Ser Phe Asn Gly Thr Glu Asn
 385 390 395 400
 Lys Leu Asn Gly Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile
 405 410 415
 Asn Met Trp Gln Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala
 420 425 430
 Gly Asn Leu Thr Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
 435 440 445
 Asp Gly Gly Lys Thr Gly Pro Asn Asp Thr Glu Ile Phe Arg Pro Gly
 450 455 460
 Gly Gly Asp Met Arg Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys
 465 470 475 480
 Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg
 485 490 495
 Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe
 500 505 510
 Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile
 515 520 525

Thr Leu Thr Val Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln
 530 535 540
 Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
 545 550 555 560
 Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Ile Leu Ala Val
 565 570 575
 Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
 580 585 590
 Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser
 595 600 605
 Asn Arg Ser His Asp Glu Ile Trp Asp Asn Met Thr Trp Met Gln Trp
 610 615 620
 Asp Arg Glu Ile Asn Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu
 625 630 635 640
 Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu
 645 650 655
 Asp Ser Trp Gln Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu
 660 665 670
 Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
 675 680 685
 Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly
 690 695 700
 Tyr Ser Pro Leu Pro Phe Gln Thr Leu Thr Pro Asn Pro Arg Glu Pro
 705 710 715 720
 Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
 725 730 735
 Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
 740 745 750
 Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
 755 760 765
 Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
 770 775 780
 Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
 785 790 795 800
 Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
 805 810 815

Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
820 825 830

Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
835 840 845

Gln

<210> 24

<211> 855

<212> PRT

<213> Human immunodeficiency virus

<400> 24

Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
20 25 30

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
65 70 75 80

Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
85 90 95

Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr
115 120 125

Asn Tyr Ser Thr Asn Tyr Ser Asn Thr Met Asn Ala Thr Ser Tyr Asn
130 135 140

Asn Asn Thr Thr Glu Glu Ile Lys Asn Cys Thr Phe Asn Met Thr Thr
145 150 155 160

Glu Leu Arg Asp Lys Lys Gln Gln Val Tyr Ala Leu Phe Tyr Lys Leu
165 170 175

Asp Ile Val Pro Leu Asn Ser Asn Ser Ser Glu Tyr Arg Leu Ile Asn
180 185 190

Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp
195 200 205

Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
 210 215 220
 Cys Lys Asn Asn Thr Ser Asn Gly Thr Gly Pro Cys Gln Asn Val Ser
 225 230 235 240
 Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Pro Leu
 245 250 255
 Leu Leu Asn Gly Ser Leu Ala Glu Gly Gly Glu Ile Ile Ile Arg Ser
 260 265 270
 Lys Asn Leu Ser Asn Asn Ala Tyr Thr Ile Ile Val His Leu Asn Asp
 275 280 285
 Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
 290 295 300
 Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Glu Asn Ile Ile
 305 310 315 320
 Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Ala Gly Glu Trp Asn
 325 330 335
 Lys Ala Val Gln Arg Val Ser Ala Lys Leu Arg Glu His Phe Pro Asn
 340 345 350
 Lys Thr Ile Glu Phe Gln Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
 355 360 365
 Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser
 370 375 380
 Lys Leu Phe Asn Ser Ser Tyr Asn Gly Thr Ser Tyr Arg Gly Thr Glu
 385 390 395 400
 Ser Asn Ser Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
 405 410 415
 Asp Met Trp Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu
 420 425 430
 Gly Asn Ile Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg
 435 440 445
 Asp Gly Gly Leu Asp Asn Ile Thr Thr Glu Ile Phe Arg Pro Gln Gly
 450 455 460
 Gly Asp Met Lys Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys Val
 465 470 475 480
 Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg
 485 490 495

Val	Val	Glu	Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Val	Ile	Phe	500	505	510
Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Asn	Met	Gly	Ala	Ala	Ser	Ile	Thr	515	520	525
Leu	Thr	Ala	Gln	Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	530	535	540
Ser	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Met	Leu	Gln	Leu	545	550	555
Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Val	Leu	Ala	Ile	Glu	565	570	575
Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly	580	585	590
Lys	Leu	Ile	Cys	Thr	Thr	Thr	Val	Pro	Trp	Asn	Ser	Ser	Trp	Ser	Asn	595	600	605
Lys	Thr	Gln	Gly	Glu	Ile	Trp	Glu	Asn	Met	Thr	Trp	Met	Gln	Trp	Asp	610	615	620
Lys	Glu	Ile	Ser	Asn	Tyr	Thr	Gly	Ile	Ile	Tyr	Arg	Leu	Leu	Glu	Glu	625	630	635
Ser	Gln	Asn	Gln	Gln	Glu	Gln	Asn	Glu	Lys	Asp	Leu	Leu	Ala	Leu	Asp	645	650	655
Ser	Arg	Asn	Asn	Leu	Trp	Ser	Trp	Phe	Asn	Ile	Ser	Asn	Trp	Leu	Trp	660	665	670
Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Ile	Gly	Leu	Arg	675	680	685
Ile	Ile	Phe	Ala	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr	690	695	700
Ser	Pro	Leu	Ser	Phe	Gln	Thr	Leu	Thr	Pro	Asn	Pro	Arg	Gly	Leu	Asp	705	710	715
Arg	Leu	Gly	Arg	Ile	Glu	Glu	Glu	Gly	Gly	Glu	Gln	Asp	Arg	Asp	Arg	725	730	735
Ser	Ile	Arg	Leu	Val	Gln	Gly	Phe	Leu	Ala	Leu	Ala	Trp	Asp	Asp	Leu	740	745	750
Arg	Ser	Leu	Cys	Leu	Phe	Ser	Tyr	His	Arg	Leu	Arg	Asp	Leu	Ile	Leu	755	760	765
Val	Thr	Ala	Arg	Val	Val	Glu	Leu	Leu	Gly	Arg	Ser	Ser	Pro	Arg	Gly	770	775	780

Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
785 790 795 800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
805 810 815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
820 825 830

Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
835 840 845

Gly Phe Glu Ala Ala Leu Gln
850 855

<210> 25

<211> 20

<212> PRT

<213> Human immunodeficiency virus

<400> 25

Asp Ile Lys Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1 5 10 15

Phe Phe Lys Thr
20

<210> 26

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 26

gacataaaac aaggaccaa agagcccttt agagactatg tagaccggtt ctttaaaacc 60

<210> 27

<211> 20

<212> PRT

<213> Human immunodeficiency virus

<400> 27

Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1 5 10 15

Phe Phe Lys Thr
20

<210> 28

<211> 47

<212> PRT

<213> Human immunodeficiency virus

<400> 28

Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
1 5 10 15

Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
20 25 30

Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
35 40 45

<210> 29

<211> 48

<212> PRT

<213> Human immunodeficiency virus

<400> 29

Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
1 5 10 15

Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
20 25 30

Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
35 40 45